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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/029,314

DATE: 02/12/2002
 TIME: 08:45:08

Input Set : N:\Crf3\RULE60\10029314.txt
 Output Set: N:\CRF3\02122002\J029314.raw

3 <110> APPLICANT: Salon et al, John A.
 5 <120> TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
 6 Receptor (MCH1) And Uses Thereof
 8 <130> FILE REFERENCE: 1795/57453-C/JPW
 10 <140> CURRENT APPLICATION NUMBER: 10/029,314
 11 <141> CURRENT FILING DATE: 2001-12-20
 13 <150> PRIOR APPLICATION NUMBER: 09/899,732
 14 <151> PRIOR FILING DATE: 2001-07-05
 16 <150> PRIOR APPLICATION NUMBER: 09/610,635
 17 <151> PRIOR FILING DATE: 2000-07-05
 19 <160> NUMBER OF SEQ ID NOS: 28
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1269
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
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 31 ggtggcaggc gctggaggct gccgcagcct gcgtgggtgg aggggagctc agctcggttgc 180
 32 tgggagcagg cgaccggcac tggctggatg gaccttggaa cctcgctgt gcggacttgt 240
 33 cccaatgcca gcaacacctc tgatggcccc gataacctca cttcagcagg atcaccttct 300
 34 cgcacgggga gcatctccta catcaacatc atcatgcctt cggtgttcgg caccatctgc 360
 35 ctccctggca tcatcgaa cttcacggtc atcttcgcgg tcgtgaagaa gtccaaagctg 420
 36 cactggtgca acaacgtccc cgacatcttc atcatcaacc tctcggtagt agatctcctc 480
 37 tttctcctgg gcatgcctt catgatccac cagctcatgg gcaatgggt gtggacttt 540
 38 ggggagacca tgtgcacccat catcacggcc atggatgcca atagtcagtt caccaggcacc 600
 39 tacatcctga ccgcattggc cattgaccgc tacctggcca ctgtccaccc catcttcc 660
 40 acgaagttcc ggaagccctc tggccacc ctggatct gcctctgtg ggccctctcc 720
 41 ttcatcagca tcaccctgt gtggctgtat gccagactca tccccttccc aggaggtgca 780
 42 gtgggctgca gcatacgccat gccaaaccca gacactgacc tctactgggt caccctgtac 840
 43 cagttttcc tggccttgc cctgccttt gtggatca cagccgcata cgtgaggatc 900
 44 ctgcagcgcata tgacgtccatc agtggccccc gcctccagc gcacatccg gctgcggaca 960
 45 aagagggtga cccgcacagc catgcctatc tggatgttgc tctttgtgt ctggcacc 1020
 46 tactatgtgc tacagctgac ccagttgtcc atcagccgc cgcacccatc ctttgttac 1080
 47 ttatacaatg cggccatcag ctgggctat gccaacagct gcctcaaccc ctttgttac 1140
 48 atcgtgtct gtgagacgtt ccgcaaacgc ttggctctgt cggtaagacc tgcagccag 1200
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 54 <211> LENGTH: 422
 55 <212> TYPE: PRT
 56 <213> ORGANISM: Homo sapiens

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 63 20 25 30
 65 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
 66 35 40 45
 68 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
 69 50 55 60
 71 Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
 72 65 70 75 80
 74 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
 75 85 90 95
 77 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
 78 100 105 110
 80 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
 81 115 120 125
 83 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
 84 130 135 140
 86 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
 87 145 150 155 160
 89 Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
 90 165 170 175
 92 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
 93 180 185 190
 95 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
 96 195 200 205
 98 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
 99 210 215 220
 101 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
 102 225 230 235 240
 104 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
 105 245 250 255
 107 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
 108 260 265 270
 110 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
 111 275 280 285
 113 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
 114 290 295 300
 116 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
 117 305 310 315 320
 119 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
 120 325 330 335
 122 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
 123 340 345 350
 125 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
 126 355 360 365
 128 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
 129 370 375 380

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131 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
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134 Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
135 405 410 415
137 Thr Glu Ser Lys Gly Thr
138 420
141 <210> SEQ ID NO: 3
142 <211> LENGTH: 1214
143 <212> TYPE: DNA
144 <213> ORGANISM: Rattus norvegicus
146 <400> SEQUENCE: 3
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148 tgccagcaac atctccgatg gccaggataa tctcacattg ccggggtcac ctccctgcac 120
149 agggagtgtc tcctacatca acatcattat gccttccgtg tttggtagcca tctgtctct 180
150 gggcatcggt ggaaactcca cggtcatctt tgctgtggtg aagaagtcca agtacactg 240
151 gtgcagcaac gtccccgaca tcttcatcat caacctctct gtgggtggatc tgctcttcct 300
152 gctgggcattg ctttcatga tccaccagct catggggAAC ggcgtctggc actttgggg 360
153 aaccatgtgc accctcatca cagccatgga cgccaaacagt cagttcaacta gcacctacat 420
154 cctgactgcc atgaccattt accgctactt ggcaccgtc caccctatct cctccaccaa 480
155 gttccggaag ccctccatgg ccaccctgtt gatctgcctc ctgtgggcgc tctccttcat 540
156 cagtttacc cctgtgtggc tctacgcccag gtcattttt ttcccgagggg gtgtgtggg 600
157 ctgtggcattc cgcctgccaa acccgacac tgacccatctc tggttcaactc tgtaccat 660
158 ttccctggcc tttgccttc cgtttgtgtt cattaccggc gcatacgtga aaatactaca 720
159 ggcgcatttgcg tcttcgggtgg ccccaacgcctc ccaacgcgcg atccggcttc ggacaaagag 780
160 ggtgacccgc acggccattt ccattctgtt ggtcttcttt gtgtgtggg caccctacta 840
161 tgtgtgcacg ctgacccagc tgtccatca cgcggccgacc ctcacgttt tctacttgta 900
162 caacgcggcc atcagcttgg gctatgctaa cagctgcctt aaccctttt tgtacatagt 960
163 gctctgtgaa acctttcgaa aacgcttggt gttgtcagtg aagcctgcag cccagggca 1020
164 gctccgcacg gtcagcaacg ctcagacacg tgatgaggag aggacagaaaa gcaaaggcac 1080
165 ctgacaattt cccagtcgccc tccaagtca ggcacccat caaacgtgg ggagagatac 1140
166 tgagattaaa cccaggcta ccctgggaga atgcagaggc tggaggctgg gggctttag 1200
167 caaccacatt ccac 1214
170 <210> SEQ ID NO: 4
171 <211> LENGTH: 353
172 <212> TYPE: PRT
173 <213> ORGANISM: Rattus norvegicus
175 <400> SEQUENCE: 4
176 Met Asp Leu Gln Thr Ser Leu Leu Ser Thr Gly Pro Asn Ala Ser Asn
177 1 5 10 15
179 Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg
180 20 25 30
182 Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
183 35 40 45
185 Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
186 50 55 60
188 Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
189 65 70 75 80
191 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
192 85 90 95

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194 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
195      100          105          110
197 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
198      115          120          125
200 Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala
201      130          135          140
203 Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala
204 145          150          155          160
206 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
207      165          170          175
209 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
210      180          185          190
212 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
213      195          200          205
215 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
216      210          215          220
218 Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala
219 225          230          235          240
221 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
222      245          250          255
224 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
225      260          265          270
227 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
228      275          280          285
230 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
231      290          295          300
233 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
234 305          310          315          320
236 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr
237      325          330          335
239 Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
240      340          345          350
242 Thr
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247 <211> LENGTH: 26
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
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255 gggaaactcca cggtcatctt cgccgt          26
258 <210> SEQ ID NO: 6
259 <211> LENGTH: 26
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
266 <400> SEQUENCE: 6
267 tagcggtaaa tggccatggc ggtcag          26

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270 <210> SEQ ID NO: 7
271 <211> LENGTH: 45
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
278 <400> SEQUENCE: 7
279 ctccctggca tgccctcat gatccaccag ctcatggca atggg 45
282 <210> SEQ ID NO: 8
283 <211> LENGTH: 25
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
290 <400> SEQUENCE: 8
291 cttcttaggcc tgtacggaag tgtta 25
294 <210> SEQ ID NO: 9
295 <211> LENGTH: 27
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
302 <400> SEQUENCE: 9
303 gttgtgggtt gtccaaactc atcaatg 27
306 <210> SEQ ID NO: 10
307 <211> LENGTH: 37
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
314 <400> SEQUENCE: 10
315 cgcgatcca ttatgtctgc actccgaagg aaatttg 37
318 <210> SEQ ID NO: 11
319 <211> LENGTH: 38
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
326 <400> SEQUENCE: 11
327 cgcgattct tatgtgaagc gatcagagtt cattttc 38
330 <210> SEQ ID NO: 12
331 <211> LENGTH: 34
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Description of Artificial Sequence: primer/probe
338 <400> SEQUENCE: 12
339 gcgggatccg ctatggctgg tgattctagg aatg 34
342 <210> SEQ ID NO: 13
  
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/029,314

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Input Set : N:\Crf3\RULE60\10029314.txt

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